

GenCore version 5.1.3  
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OM protein - nucleic search, using frame\_plus.f2a model

Run on: January 16, 2003, 16:55:57 : Search time 440.224 Seconds  
(without alignments)  
330.553 Million cell updates/sec

Title: us-09-856-070-25  
Perfect score: 23  
Sequence: 1 MRLQ 5

Scoring table: HUSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Egapop 6.0 , Egapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters 4109280

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODE=frame\_plus\_model -DEV=exp  
-Q=Zcpn2\_1/USUM62 -SPOT=us09856070/ranat\_14012004 -seq 4 10 21/seq -query fasta\_1\_1592  
-DB=GenEmbl -QEXT=lastap -SUFFIX=rge -MINMATCH=0 1 -L=exp -n -L=expEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40 -odi -LIST=45  
-DOCALIGN=200 -THP\_SCOPE=act -THP\_MAX=100 -THP\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OFFPRM=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USUR=US09856070/ranat\_14012004 -seq 4 10 21/seq -query fasta\_1\_1592 -n -L=exp -n -L=expEXT=0  
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-YGAPOP=10 -YGAPEXT=0 5 -DELAP=6 -DELEXT=7

Database: GenEmbl:  
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9: gb\_pl:\*  
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11: gb\_pl:\*  
12: gb\_pl:\*  
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32: em\_hiq\_other:\*  
33: em\_hiq\_mus:\*  
34: em\_hiq\_pln:\*  
35: em\_hiq\_rnd:\*  
36: em\_hiq\_mam:\*  
37: em\_hiq\_vrt:\*  
38: em\_sy:\*  
39: em\_hiqo\_hum:\*  
40: em\_hiqo\_mus:\*  
41: em\_hiqo\_other:\*

pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	24	100.0	48	5	145599	106509 Sequence 13
2	23	100.0	51	6	AX161387	AX161387 Sequence
3	23	100.0	51	6	AX284883	AX284883 Sequence
4	23	100.0	91	6	AX135207	AX135207 Sequence
5	23	100.0	91	6	AX135398	AX135398 Sequence
6	23	100.0	123	11	C44283	C44283 WIAF-3913-S
7	23	100.0	129	6	AX435708	AX435708 Sequence
8	23	100.0	150	11	G65968	G65968 sy806 Misc
9	23	100.0	173	6	AX135383	AX135383 Sequence
10	23	100.0	176	8	ASA012135	AJ012135 Avena sat
11	23	100.0	180	9	HAI9292	AJ292928 Homo sapi
12	23	100.0	186	11	G33552	G33552 A09G06 Hum
13	23	100.0	206	4	TN143720	A113720 Tapirus i
14	23	100.0	209	4	AF103045	A103045 Sus scrof
15	23	100.0	212	11	G26672	G26672 human STS S
16	23	100.0	228	4	AF191705	AF191705 Equus cab
17	23	100.0	232	9	BC067309	BC067309 Rat1000r1a
18	23	100.0	248	9	HS11603F	264391 H.sapiens C
19	23	100.0	250	11	G15571	G15571 human STS S
20	23	100.0	255	6	AX211025	AX211025 Sequence
21	23	100.0	256	6	AP101898	AP101898 Sequence
22	23	100.0	259	6	AX341548	AX341548 Sequence
23	23	100.0	260	6	AX340012	AX340012 Sequence
24	23	100.0	267	6	AX436553	AX436550 Sequence
25	23	100.0	272	11	A0927756	A0927756 Rattus no
26	23	100.0	283	9	HS11604R	264392 H.sapiens C
27	23	100.0	285	6	AX074528	AX074528 Sequence
28	23	100.0	298	6	AR101915	AR101915 Sequence
29	23	100.0	306	14	GPA275895	AJ275895 Human tro
30	23	100.0	308	4	BTMSA152	X71545 H.taurus mi
31	23	100.0	308	6	AR101907	AR101907 Sequence
32	23	100.0	308	11	G75029	G75029 MARC 14187-
33	23	100.0	310	6	AX345388	AX345388 Sequence
34	23	100.0	311	11	HSA0441P1	H51579 H.sapiens (
35	23	100.0	315	6	AX314014	AX314014 Sequence
36	23	100.0	319	11	GI3974	GI3974 human STS S
37	23	100.0	321	11	HS900E8T	AL032600 H.sapiens
38	23	100.0	322	9	HS14711R	256840 H.sapiens C
39	23	100.0	330	6	AX187767	AX187767 Sequence
40	23	100.0	333	8	TORCP1R1	M16869 Tobacco Scr
41	23	100.0	341	11	HSPA3A43	794244 H.sapiens f
42	23	100.0	351	11	G57946	G57946 SHGC-103923
43	23	100.0	352	9	HS031734	U11734 Homo sapien
44	23	100.0	353	11	AUF26228	AUF26228 Rattus no
45	23	100.0	356	11	HSA154ZD1	267351 H.sapiens D

ALIGNMENTS

RESULT 1

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106509
LOCUS      106509               36 bp      DNA      Linear      PAT 02-DEC-1994
DEFINITION Sequence 13 from Patent WO 9002798.
ACCESSION  106509
VERSION    106509.1  GI:589567
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 36)
AUTHORS   Anderson,S., Bennett,W.F., Botstein,D., Higgins,D.L., Paoni,N.F.
          and Zoller,M.
TITLE     TISSUE PLASMINOGEN ACTIVATOR HAVING 77%-GENIC OF FIBRIN SPECIFIC
          PROPERTIES
JOURNAL    Patent: WO 9002798-A 13 22-MAR-1990.
FEATURES   Location/Qualifiers
            source          1..36
                        /organism="unknown"
BASE COUNT  9 a  7 c  8 g  12 t
ORIGIN
Alignment Scores:
Pred. No.:      48.9      Length:      36
Score:          23.00     Matches:      5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    100.00% Indels:      0
DB:             6        Gaps:        0

US-09-856-070-25 (1-5) x 106509 (1-36)

QY      1  MetLeuArgLeuGln 5
DB      15  ATGCTGGCAGCTGCAA 29

RESULT 2
AX161287
LOCUS      AX161287               51 bp      DNA      Linear      PAT 22-JUN-2001
DEFINITION Sequence 4615 from Patent WO0140521.
ACCESSION  AX161287
VERSION    AX161287.1  GI:14542618
KEYWORDS   human.
SOURCE     Homo sapiens
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE  1 (bases 1 to 51)
AUTHORS   Shimkels,R.A. and Leach,M.
TITLE     Nucleic acids containing single nucleotide polymorphisms and
          methods of use thereof
JOURNAL    Patent: WO 0140521-A 4615 07-JUN-2001;
          Curagen Corporation (US)
FEATURES   Location/Qualifiers
            source          1..51
                        /organism="Homo sapiens"
            misc-feature     26
                        db_xref="taxon:9606"
BASE COUNT  11 a  15 c  14 g  11 t
ORIGIN
Alignment Scores:
Pred. No.:      70.1      Length:      51
Score:          23.00     Matches:      5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    100.00% Indels:      0
DB:             6        Gaps:        0

US-09-856-070-25 (1-5) x AX161287 (1-51)

QY      1  MetLeuArgLeuGln 5

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DB      18  ATGCTAGGCTACAG 32

RESULT 3
AX284883
LOCUS      AX284883               51 bp      DNA      Linear      PAT 20-NOV-2001
DEFINITION Sequence 688 from Patent WO0179556.
ACCESSION  AX284883
VERSION    AX284883.1  GI:17045571
KEYWORDS   human.
SOURCE     Homo sapiens
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE  1
AUTHORS   Ellis,J., Brown,J.L., Holt,A. and van Huffel,C.
TITLE     Novel genes, compositions and methods for the identification,
          assessment, prevention, and therapy of human cancers
JOURNAL    Patent: WO 0179556-A 688 25-OCT-2001;
          Millennium Predictive Medicine, Inc. (US)
FEATURES   Location/Qualifiers
            source          1..51
                        /organism="Homo sapiens"
                        /db_xref="taxon:9606"
BASE COUNT  10 a  15 c  16 g  10 t
ORIGIN
Alignment Scores:
Pred. No.:      70.1      Length:      51
Score:          23.00     Matches:      5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    100.00% Indels:      0
DB:             6        Gaps:        0

US-09-856-070-25 (1-5) x AX284883 (1-51)

QY      1  MetLeuArgLeuGln 5
DB      19  ATGCTCAGGCTTCAG 33

RESULT 4
AX135207
LOCUS      AX135207               91 bp      DNA      Linear      PAT 29-MAY-2001
DEFINITION Sequence 15 from Patent WO0132928.
ACCESSION  AX135207
VERSION    AX135207.1  GI:14271556
KEYWORDS   human.
SOURCE     Homo sapiens
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE  1 (bases 1 to 91)
AUTHORS   Farr,S.
TITLE     Methods of determining individual hypersensitivity to an agent
          Patent: WO 0132928-A 15 10-MAY-2001;
          Phase 1 Molecular Toxicology Inc. (US)
FEATURES   Location/Qualifiers
            source          1..91
                        /organism="Homo sapiens"
                        /db_xref="taxon:9606"
BASE COUNT  19 a  33 c  11 g  28 t
ORIGIN
Alignment Scores:
Pred. No.:      127      Length:      91
Score:          23.00     Matches:      5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    100.00% Indels:      0
DB:             6        Gaps:        0

US-09-856-070-25 (1-5) x AX135207 (1-91)

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QY 1 MetLeuArdLeuGln 5
|||||
Db 33 ATGCTCAGGCTTCAA 47

RESULT 5
AX135398/c
LOCUS AX135398 91 bp DNA linear PAT 29-MAY-2001
DEFINITION Sequence 206 from patent WO0229113
ACCESSION AX135398
VERSION AX135398.1 GI:14271747
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 91)
AUTHORS Farr,S.
TITLE Methods of determining individual hypersensitivity to an agent
JOURNAL Patent: WO 0132928-A 2001-05-10
PHASE 1 Molecular Toxicology Inc. (US)
FEATURES
Source Location/Qualifiers
1..91
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 28 a 11 c 33 g 19 t
ORIGIN

Alignment Scores:
Pred. No.: 127 Length: 91
Score: 23.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-856-070-25 (1-5) x AX135398 (1-91)

QY 1 MetLeuArdLeuGln 5
|||||
Db 59 ATGCTCAGGCTTCAA 45

RESULT 6
G44283
LOCUS G44283 123 bp DNA linear STS 28-JAN-1999
DEFINITION WIAP-3933-STS Human Hudson SANGER Homo sapiens STS genomic,
sequence tagged site.
ACCESSION G44283
VERSION G44283.1 GI:4193209
KEYWORDS STS.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 123)
AUTHORS Wang,D.G., Fan,T.B., Siao,C.T., Berne,A., Young,P., Sapolsky,P.,
Chandour,G., Perkins,N., Winchester,E., Spencer,J., Kruglyak,L.,
Stein,L., Hsieh,L., Topaloglou,I., Hubbell,E., Robinson,E.,
Mittman,M., Morris,M.S., Shen,N., Kilburn,D., Rioux,J.,
Nusbaum,C., Rozen,S., Hudson,T.I., Lipshutz,P., Chee,M. and
Lander,E.S.
TITLE Large-scale identification, mapping, and genotyping of
single-nucleotide polymorphisms in the human genome
JOURNAL Science 280 (5360), 1377-1382 (1998)
MEDLINE 98248615
PUBMED 9582121
SYNOPSIS STS328822
CONTACT: Thomas Hudson
Whitehead Institute/MIT Center for Genome Research
Whitehead Institute for Biomedical Research
9 Cambridge Center, Cambridge MA 02142 USA
Tel: 617 252 1900
Fax: 617 252 1902

Email: thudson@genome.wi.mit.edu
Primer A: TGGAGGCTCACTTGAGC
Primer B: ATGCTCAGGCTTCAATTC
STS size: 123
PCR Profile:
Presoak: 94 degrees C for 4.00 minutes
Denaturation: 94 degrees C for 50.0 seconds
Annealing: 58 degrees C for 1.50 minutes
Polymerization: 72 degrees C for 5.00 minutes
PCR Cycles: 30
Thermal Cycler: custom built by IAS, Costa, Cambridge MA

Protocol:
Template: 10 ng
Primer: each 5 pM
dNTPs: 4 mM
lag Polymerase: 0.5 U
Total Vol: 20 ul.

Buffer:
Mg2+: 1.5 mM
KCl: 50 mM
Tris-HCl: 10 mM
Gelatin: .001 %
Location/Qualifiers
1..123
/organism="Homo sapiens"
/db_xref="taxon:9606"
/map="164.70 cM from top of Chr9 linkage group"
/clone_lib="Human Hudson SANGER"
/note="human STS created from EST in the Sanger database"
1..123
primer_bind 1..18
primer_bind complement(104..123)
BASE COUNT 40 a 30 c 30 g 22 t 1 others
ORIGIN

Alignment Scores:
Pred. No.: 174 Length: 123
Score: 23.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 11 Gaps: 0

US 09 856-070-25 (1-5) x G44283 (1-123)

QY 1 MetLeuArdLeuGln 5
|||||
Db 24 ATGCTCAGGCTTCAA 38

RESULT 7
AX435708
LOCUS AX435708 129 bp DNA linear PAT 29-JUN 2002
DEFINITION Sequence 4123 from Patent WO0229113.
ACCESSION AX435708
VERSION AX435708.1 GI:21660516
KEYWORDS
SOURCE Bacillus licheniformis.
ORGANISM Bacillus licheniformis
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
REFERENCE 1
AUTHORS Berka,R. and Clausen,I.G.
TITLE Methods for monitoring multiple gene expression
JOURNAL Patent: WO 0229113-A 4123 11-Apr 2002
SYNOPSIS Novozymes Biotech, Inc. (US) ; Novozymes A/S (DK)
FEATURES
Source Location/Qualifiers
1..129
/organism="Bacillus licheniformis"
/db_xref="taxon:1402"
BASE COUNT 27 a 40 c 29 g 33 t
ORIGIN

Alignment Scores:

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Pred. No.: 184 Length: 129
Score: 23.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-856-070-25 (1-5) x AX135709 (1-129)

QY 1 MetLeuArqLeuGln 5
DB 66 AGGTTACGACTTCAAA 80

RESULT 8
LOCUS G65968 150 bp DNA Linear STS 02-NOV-2001
DEFINITION sY806 Miscellaneous Y sequences Homo sapiens STS genomic, sequence
tagged site.
ACCESSION G65968
VERSION G65968.1 GI:15078019
KEYWORDS STS
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 150)
AUTHORS Tillord, G.A., Kurenda-Kawauchi, T., Skajet, S., H., Pozen, S.,
Brown, L.G., Rosenborg, M., McPherson, T.D., Wylie, K., Sekhon, M.,
Kucaba, T.A., Waterston, R.H., and Page, D.C.
TITLE A physical map of the human Y chromosome
JOURNAL Nature 409 (6822), 943-945 (2001)
MEDLINE 21131744
PubMed 11237016
COMMENT
Contact: Tomoko Kawauchi
Page Lab
Whitehead Institute for Biomedical Research
Room 423, 9 Cambridge Center, Cambridge, MA 02142, USA
Email: kawauchi@wi.mit.edu
Primer A: TGTAAGTGAAGGAGGAGGTCGG
Primer B: AGGAAACAAAGGAGAGCATTCG
STS size: 150
PCR Profile:
94C 3:00 min
45x / 94C 1:00 sec
55x 1:00 min
72C 1:00 min
72C 5:00 min
Protocol:
Template: 1 ul saturated bacterial culture (HACs) or 100
ng DNA
Primer: each 1 uM
dNTPs: each 100 uM
Taq Polymerase: 0.05 units/ul
Total Vol: 15 ul or 20 ul
Mineral Oil: 15 ul

Buffer:
Stock Reagent Volume Mixed Final Conc. of 10x Stock
1M KCl 10 ml 500 mM
1M Tris-HCl, pH 9.0 2 ml 100 mM
Triton X-100 200 ul 1.0 %
2M MgCl2 150 ul 15 mM
H2O 7.65 ml.

FEATURES
Source
1..150
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Miscellaneous Y sequences"
/notes="Human STS derived from miscellaneous Y sequences"
STS
1..150
primer_bind
1..20

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primer_bind 38 a 26 c 43 g 43 t
BASE COUNT complement(130..150)
ORIGIN
Alignment Scores:
Pred. No.: 213 Length: 150
Score: 23.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 11 Gaps: 0

US-09-856-070-25 (1-5) x G65968 (1-150)

QY 1 MetLeuArqLeuGln 5
DB 94 ATTGTGAATTAAAG 80

RESULT 9
LOCUS AX135383 173 bp DNA Linear PAT 29-MAY 2001
DEFINITION Sequence 191 from Patent WO9132928.
ACCESSION AX135383
VERSION AX135383.1 GI:14271712
KEYWORDS human.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 173)
AUTHORS Farr, S.
TITLE Methods of determining individual hypersensitivity to an agent
JOURNAL Patent: WO 0132928-A 191 10-MAY-2001;
Phase-1 Molecular Toxicology Inc. (US)
FEATURES
Source
1..173
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 59 a 25 c 40 g 49 t
ORIGIN
Alignment Scores:
Pred. No.: 247 Length: 173
Score: 23.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-856-070-25 (1-5) x AX135383 (1-173)

QY 1 MetLeuArqLeuGln 5
DB 67 AAGCTGGCGCTTCAAA 81

RESULT 10
LOCUS ASA012135/c 176 bp DNA Linear PIN 05-JAN 2001
DEFINITION Avena sativa mitochondrial cp-like tRNA-Ser (GGA) gene.
ACCESSION AJ012135
VERSION AJ012135.1 GI:12057053
KEYWORDS transfer RNA-Ser; tRNA-Ser gene.
SOURCE cat.
ORGANISM Mitochondrion Avena sativa
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooidae; Aveneae; Avena.
REFERENCE 1 (bases 1 to 176)
AUTHORS Rainaldi, G.
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 176)
AUTHORS Rainaldi, G.
TITLE Direct Submission

```

JOURNAL Submitted (14-OCT-1998) Rainaldi G., Dipartimento di Biochimica e Biologia Molecolare, Universita' di Bari, via Grubona 4, 70125 BARI, ITALY

FEATURES  
 source Location/Qualifiers  
 1..176  
 /organism="Avena sativa"  
 /organelle="mitochondrion"  
 /db\_xref="taxon:4498"  
 57..143  
 /gene="tRNA-Ser (GCA)"  
 57..143  
 /gene="tRNA-Ser (GCA)"  
 /product="tRNA-Ser"  
 /evidence experimental

BASE COUNT 48 a 32 c 42 g 54 t

ORIGIN

Alignment Scores:  
 Pred. No.: 252 Length: 176  
 Score: 23.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 8 Gaps: 0

US-09-856-070-25 (1-5) x ASA012135 (1-176)

QY 1 MetLeuArgLeuGln 5  
 |||||

Db 89 ATGCTAGCGCTTCAA 75

RESULT 11

HAJ9282 180 bp DNA linear PRI 04-NOV-1998  
 LOCUS HAJ9282/2  
 DEFINITION Homo sapiens translocation t(11;22) DNA in twings's tumor derivative 11 (isolate: EWTUM23/cha).

ACCESSION AJ229282  
 VERSION AJ229282.1 GI:3849897  
 KEYWORDS EWS; FLI-1; translocation.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 180)  
 AUTHORS Zucman-Rossi, J., Lejoux, F., Virelizier, J. M., Leary, B. and Thomas, J.  
 TITLE Chromosome translocation based on illegitimate recombination in human tumors  
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 95 (20), 11786-11791 (1998)  
 MEDLINE 98426231  
 PUBMED 9751743  
 REFERENCE 2 (bases 1 to 180)  
 AUTHORS Zucman-Rossi, J.  
 TITLE Direct Submission  
 JOURNAL Submitted (27 MAY 1998) Zucman-Rossi J., INSERM U434/CEPH, 27 rue Juliette Lodu, 75010 Paris, FRANCE

FEATURES  
 source Location/Qualifiers  
 1..180  
 /organism="Homo sapiens"  
 /isolate="EWTUM23/cha"  
 /db\_xref="taxon:9606"  
 /tissue.type="cwing's tumor"  
 /note="derivative 11"  
 1..103  
 /gene="FLI-1"  
 1..103  
 /gene="FLI-1"  
 /note="Y17293; location 44761-44863"  
 106..180  
 /gene="EWS"  
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 /gene="EWS"  
 /note="Y08806; location 39688-39762"

BASE COUNT 55 a 22 c 44 g 59 t

ORIGIN

Alignment Scores:  
 Pred. No.: 257 Length: 180  
 Score: 23.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 9 Gaps: 0

US-09-856-070-25 (1-5) x HAJ9282 (1-180)

QY 1 MetLeuArgLeuGln 5  
 |||||

Db 74 ATGTTAGATTACAG 60

RESULT 12

G12522 185 bp DNA linear S1S 4-Sep-1999  
 LOCUS G12522  
 DEFINITION AG090066 Human HOMO sapiens STS genomic, sequence tagged site.  
 ACCESSION G12522  
 VERSION G12522.1 GI:5923043  
 KEYWORDS STS.  
 SOURCE Homo sapiens.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 186)  
 AUTHORS Adams, M.D.  
 TITLE Human STS sequences  
 JOURNAL Unpublished (1996)  
 COMMENT Contact: Mark Adams  
 The Institute for Genomic Research  
 5712 McLean Center Dr., Rockville, MD 20850  
 Email: mdadams@tigr.org  
 Primer A: AGTACGGTTACAGGTATATCTC  
 Primer B: AGTGGATCAAGCCCTGTA  
 STS size: 186  
 PCR Profile:  
 Denaturation: 96C 5min  
 Anneal: 54C 30sec  
 Extend: 72C 30sec  
 Denature: 95C 30sec  
 FinalExtend: 72C 5min  
 Cycles: 30  
 Protocol:  
 GenomicDNA: 25 ng  
 Primer: 0.43 uM each  
 dNTPs: 230 uM each  
 AmpliTaq: 0.5 units  
 TaqStart Ab: 0.5 units  
 Total Volume: 10 uL  
 Buffer:  
 Tris-HCl pH8.8: 100 mM  
 KCl: 500 mM  
 MgCl2: 20 mM  
 Triton X-100: 1%  
 Concentration: 10X  
 Prepared with primer pairs derived from H0C112360, GenBank  
 Accession Numbers: P57885, R2414, L65722.  
 FEATURES  
 source Location/Qualifiers  
 1..186  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone\_lib="Human"  
 1..186  
 primer\_bind 1..23  
 primer\_bind complement(169..186)  
 primer\_bind 35 a 48 c 37 g 66 t  
 BASE COUNT 35 a 48 c 37 g 66 t  
 ORIGIN

```

Alignment Scores:
  Pred. No.:      266      Length:      186
  Score:          24.00    Matches:      5
  Percent Similarity: 100.00%  Conservative: 0
  Best Local Similarity: 100.00%  Mismatches: 0
  Query Match:      100.00%  Indels:      0
  DB:              11      Gaps:      0

US-09-856-070-25 (1-5) x G132522 (1-186)

QY 1 MetLeuArqLeuGln 5
  |||||
DB 159 ATGCTGCGATACAA 174

RESULT 13
LOCUS      TINI33720          206 bp  mRNA  linear  MAR 15 SEP 1999
DEFINITION Tapirus indicus mRNA for MHC class I antigen, clone TAP1.
ACCESSION  AJ133720
VERSION    AJ133720.1 GI:4538864
KEYWORDS   major histocompatibility complex, MHC class I antigen.
SOURCE     Tapirus indicus.
ORGANISM   Tapirus indicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Perissodactyla; Tapiridae; Tapirus.
REFERENCE  1 (bases 1 to 206)
AUTHORS    Holmes, F. C. and Ellis, S. A
TITLE      Evolutionary history of MHC class I genes in the mammalian order
            Perissodactyla
JOURNAL    J. Mol. Evol. 49 (3), 316-324 (1999)
MEDLINE    99406857
PUBMED     10473772
REFERENCE  2 (bases 1 to 206)
AUTHORS    Ellis, S. A.
TITLE      Direct Submission
JOURNAL    Submitted (12-MAR-1999) Ellis S.A., Deptt of Immunology, Institute
            for Animal Health, Compton, RG20 7NN, UNITED KINGDOM
FEATURES   Location/Qualifiers
            1..206
            /organism="Tapirus indicus"
            /db_xref="taxon:9802"
            /clone="TAP1"
            /cell_type="lymphocyte"
            /function="antigen presenting molecule"
            /codon_start=4
            /product="MHC class I antigen"
            /protein_id="CAH19536.1"
            /db_xref="GI:4538865"
            /translation="PPQSTIPWGIIVLWLCVVVSANVAGVMMPKPKSGTQPS
            SYATASSDSNAQSDVSLDPKV"
BASE COUNT  40 a 49 c 68 q 49 t
ORIGIN
1
206

CDS
1..206
/translation="antigen presenting molecule"
/codon_start=4
/product="MHC class I antigen"
/protein_id="CAH19536.1"
/db_xref="GI:4538865"

Alignment Scores:
  Pred. No.:      296      Length:      206
  Score:          24.00    Matches:      5
  Percent Similarity: 100.00%  Conservative: 0
  Best Local Similarity: 100.00%  Mismatches: 0
  Query Match:      100.00%  Indels:      0
  DB:              4      Gaps:      0

US 09 856 070-25 (1-5) x TINI33720 (1-206)

QY 1 MetLeuArqLeuGln 5
  |||||
DB 139 ATGCTGCGATACAA 154

RESULT 14
LOCUS      AF103945          209 bp  mRNA  linear  MAR 09-MAR-1999
DEFINITION Sus scrofa CCAAT/enhancer binding protein beta (C/EBP beta) mRNA.
partial cds.
ACCESSION  AF103945
VERSION    AF103945.1 GI:4378474
KEYWORDS   Sus scrofa
SOURCE     Sus scrofa
            Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
REFERENCE  1 (bases 1 to 209)
AUTHORS    Ding, S. T. and Mersmann, H. J.
TITLE      Direct Submission
JOURNAL    Submitted (03-NOV-1998) Pediatrics, Baylor College of Medicine,
            1100 Bates St., Houston, TX 77030, USA
FEATURES   Location/Qualifiers
            1..209
            /organism="Sus scrofa"
            /db_xref="taxon:9823"
            /cl_2209
            /gene="C/EBP beta"
            /cl_2209
            /gene="C/EBP beta"
            /codon_start=2
            /product="CCAAT/enhancer binding protein beta"
            /protein_id="AA019576.1"
            /db_xref="GI:4378475"
            /translation="KKIVKKSQFYKIKKLNNAVAKSHKAKMKNLTKQKVLFLI
            AENERLQKKVEQISRELSLRLNLFK"
BASE COUNT  59 a 59 c 69 q 22 t
ORIGIN
1
209

Alignment Scores:
  Pred. No.:      300      Length:      209
  Score:          24.00    Matches:      5
  Percent Similarity: 100.00%  Conservative: 0
  Best Local Similarity: 100.00%  Mismatches: 0
  Query Match:      100.00%  Indels:      0
  DB:              4      Gaps:      0

US-09-856-070-25 (1-5) x AF103945 (1-209)

QY 1 MetLeuArqLeuGln 5
  |||||
DB 115 ATGCTGCGATACAA 101

RESULT 15
LOCUS      G26672          212 bp  DNA  linear  STS 02-JUN-1996
DEFINITION human STS STS_M63154, sequence tagged site.
ACCESSION  G26672
VERSION    G26672.1 GI:1348904
KEYWORDS   STS; STS sequence; primer; sequence tagged site.
SOURCE     Homo sapiens STSs derived from sequences in dbEST and the UniGene
            collection.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE  1 (bases 1 to 212)
AUTHORS    Hudson, T.
TITLE      Whitehead Institute/MIT Center for Genome Research; Physically
            Mapped STSs
JOURNAL    unpublished (1995)
COMMENT    Contact: Thomas Hudson
            Whitehead Institute/MIT Center for Genome Research
            Whitehead Institute for Biomedical Research
            9 Cambridge Center, Cambridge MA 02142 USA
            tel: 617 252 1900
            fax: 617 252 1902
            Email: thudson@genome.wi.mit.edu
            Primer A: TGGGTCAGCTTCTATCAAA
            Primer B: ATGAGTCATAGATGTGACATCCA
            STS size: 178

```

PCR Profile:

Presoak:  
Denaturation:  
Annealing: 56 degrees C  
Polymerization:  
PCR Cycles: 35  
Thermal Cycler:

Protocol:

Template: 10 ng  
Primer: each 5 pM  
dNTPs: each 4 mM  
Taq Polymerase: 0.025 units/ul  
Total Vol: 20 ul

Buffer:

MgCl2: 1.5 mM  
KCl: 50 mM  
Tris-HCl: 10 mM  
pH: 9.3

Derived from dREST (genbank accession M63154).

FEATURES  
source  
1..212  
Location/Qualifiers  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/map="317.2 cR from top of Chr11 linkage group"  
STS  
primer\_bind  
12..189  
primer\_bind  
12..133  
complement(165..189)  
BASE COUNT 75 a 40 c 35 g 62 t  
ORIGIN

Alignment Scores:

Pred. No.:	305	Length:	212
Score:	23.00	Matches:	5
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	11	Gaps:	0

US-09-856-070-25 (1-5) x 326672 (1 212)

OY 1 MetLeuArgLeuGln 5

|||||

Db 178 ATTTGAGACTCCAG 164

Search completed: January 16, 2003, 19:05:57  
Job time : 443.214 secs

